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659	GAGGCATCAGACTATAAAGATTCTCTATATTTGTGTAAATGGATCATCAGAGAACAAGCCT	718
203	GluAlaSerAspTyrLysAspPheTyrIleCysValAsnGlySerSerGluAsnLysPro	222
719	ATCAGATCCAGTTATTTACACTTTTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGTC	778
223	IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleValLysProLeuProVal	242
779	TATCTTACTTTTACTCGGAGAGTTTCATGTGAAATTAAGCTGAAATGGAGCATACTTTTG	838
243	TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuLysTrpSerIleProLeu	262
839	GGACCTATTCCAGCAAGGTGTTTGTATTATGAAATTGAGATCAGAGAAGATGATACTACC	898
263	GlyProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspThrThr	282
899	TTGGTGACTGCTACAGTTGAAATGAAACATACACCTTGAAACAAACAATGAAACCCGA	958
283	LeuValThrAlaThrValGluAsnGluThrTyrThrLeuLysThrThrAsnGluThrArg	302
959	CAATTATGCTTTGTAGTAAGAAGCAAAAGTGAATATTTATTGCTCAGATGACGGAATTTGG	1018
303	GlnLeuCysPheValValArgSerLysValAsnIleTyrCysSerAspAspGlyIleTrp	322
1019	AGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGCTA	1078
323	SerGluTrpSerAspLysGlnCysTrpGluGlyGluAspLeuSerLysLysThrLeuLeu	342
1079	CGTTTCTGGCTACCATTTTGGTTTCATCTTAATATTAGTTATATTTGTAAACCGTCTGCTT	1138
343	ArgPheTrpLeuProPheGlyPheIleLeuIleLeuValIlePheValThrGlyLeuLeu	362
1139	TTGCGTAAGCCAAACACCTACCCAAAAATGATTCAGAAATTTTCTGTGATACATGAAGA	1198
363	LeuArgLysProAsnThrTyrProLysMetIleProGluPhePheCysAspThr	381 380
1199	CTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATGGCCAAATGTTCA	1258
1259	ATATGAGTCTCAATAAACTGAATTTTCTTCCGGAATGTTG	1298

FIG. 2a(continuation) B

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